

SEQUENCE LISTING

<110> Liaw, Chen W.
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Leonard, James N.
Ortuno, Daniel
Lin, I-Lin

<120> Endogenous And Non-Endogenous, Constitutively Activated G Protein-Coupled Receptors

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<170> PatentIn version 3.1

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Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Asn Thr Ile Cys Tyr
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Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe
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Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
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Val Met Thr Gly Leu Trp Ile Phe Thr Ile Val Leu Thr Leu Pro Asn
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Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn
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Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile
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Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile
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Ala Ala Lys Ile His Arg Asn His Met Ile Lys Ser Ser Arg Pro Leu
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Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
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Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu
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Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe
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Met Gly Arg Asn Phe Gln Glu Arg Leu Ile Arg Ser Leu Pro Thr Ser
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Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
100 105 110

Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
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Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
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Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
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Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
165 170 175

Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
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Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
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Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
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Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
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Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
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His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
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Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
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Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
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Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
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Phe Leu Gly Asn Thr Val Val Cys Ile Ile Val Tyr Gln Arg Pro Ala
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Met Arg Ser Ala Ile Asn Leu Leu Leu Ala Thr Leu Ala Phe Ser Asp
65 70 75 80

Ile Met Leu Ser Leu Cys Cys Met Pro Phe Thr Ala Val Thr Leu Ile
85 90 95

Thr Val Arg Trp His Phe Gly Asp His Phe Cys Arg Leu Ser Ala Thr
100 105 110

Leu Tyr Trp Phe Phe Val Leu Glu Gly Val Ala Ile Leu Leu Ile Ile
115 120 125

Ser Val Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp Lys Leu Asn
130 135 140

Pro Arg Arg Ala Lys Val Ile Ile Ala Val Ser Trp Val Leu Ser Phe
145 150 155 160

Cys Ile Ala Gly Pro Ser Leu Thr Gly Trp Thr Leu Val Glu Val Pro
165 170 175

Ala Arg Ala Pro Gln Cys Val Leu Gly Tyr Thr Glu Leu Pro Ala Asp
180 185 190

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Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
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Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
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Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
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Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
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Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
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Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
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Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
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Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
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Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
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Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
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Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
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Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys		
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Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala		
	690	695
Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp		
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Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr		
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Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
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Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
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Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro
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Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
 100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln
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Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu
 130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly
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Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala
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Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser
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His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu

205

Glu Arg Cys Ile Ile Lys Ile Ser Pro Asp Leu Pro Asp Thr Ile Tyr
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Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
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Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
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Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
 145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
 165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
 180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
 195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
 210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
 225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
 245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
 260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly
355 360

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<212> DNA
<213> Homo sapiens

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tgtgccacat acctgctgat ctctgtgttg ggcgctgttg gcaatgggct gacctgtctg 180
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<210> 14
 <211> 403
 <212> PRT
 <213> Homo sapiens

<400> 14

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Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe
 35 40 45

Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg
 50 55 60

His Lys Ala Met Arg Thr Pro Thr Asn Tyr Tyr Leu Phe Ser Leu Ala
 65 70 75 80

Val Ser Asp Leu Leu Val Leu Leu Val Gly Leu Pro Leu Glu Leu Tyr
 85 90 95

Glu Met Trp His Asn Tyr Pro Phe Leu Leu Gly Val Gly Gly Cys Tyr
 100 105 110

Phe Arg Thr Leu Leu Phe Glu Met Val Cys Leu Ala Ser Val Leu Asn
 115 120 125

355

360

365

Met Thr Thr Gly Ser Thr Leu Cys Asp Val Gly Ser Leu Gly Ser Trp
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Asp Pro Ser

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<211> 930

<212> DNA

<213> Homo sapiens

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<211> 309

<212> PRT

<213> Homo sapiens

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35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
115 120 125

Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
130 135 140

Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145 150 155 160

Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Arg Phe Pro
165 170 175

Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
180 185 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
195 200 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu

210 215 220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
 225 230 235 240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
 245 250 255

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
 260 265 270

Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
 275 280 285

Leu Ala Val Ala Pro Arg Ala Lys Ala His Lys Ser Gln Asp Ser Leu
 290 295 300

Cys Val Thr Leu Ala
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 <211> 1446
 <212> DNA
 <213> Homo sapiens

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 cagagccgat ccaagagggg caccgaggat gaggaggcca agggcgtgca gcagtatgtg 180
 cctgaggagt gggcggagta cccccggccc attcaccttg ctggcctgca gccaaccaag 240
 cccttgggtg ccaccagccc taaccccgcac aaggatgggg gcaccccaga cagtgggcag 300
 gaactgaggg gcaatctgac aggggcacca gggcagaggc tacagatcca gaaccccctg 360
 tatccggtga ccgagagctc ctacagtgcc tatgccatca tgcttctggc gctggtggtg 420
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 ctgaagagcg cctggaactc catccttgcc agcctggccc tctgggattt tctggtcctc 540
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 gtttcttgct gtgccgtgcc cttcatggag gtctcctctc tgggagtcac gactttcagc 660
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<212> PRT
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Val Gly Leu Ser Arg Val Ser Gly Gly Ala Pro Leu His Leu Gly Arg
          20          25          30

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His Arg Ala Glu Thr Gln Glu Gln Gln Ser Arg Ser Lys Arg Gly Thr
          35          40          45

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Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp
          50          55          60

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Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys
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Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro
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Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln
100 105 110

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr
115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly
130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr
145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp
165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile
180 185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe
195 200 205

Met Glu Val Ser Ser Leu Gly Val Thr Thr Phe Ser Leu Cys Ala Leu
210 215 220

Gly Ile Asp Arg Phe His Val Ala Thr Ser Thr Leu Pro Lys Val Arg
225 230 235 240

Pro Ile Glu Arg Cys Gln Ser Ile Leu Ala Lys Leu Ala Val Ile Trp
245 250 255

Val Gly Ser Met Thr Leu Ala Val Pro Glu Leu Leu Leu Trp Gln Leu
260 265 270

Ala Gln Glu Pro Ala Pro Thr Met Gly Thr Leu Asp Ser Cys Ile Met
275 280 285

Lys Pro Ser Ala Ser Leu Pro Glu Ser Leu Tyr Ser Leu Val Met Thr
290 295 300

Tyr Gln Asn Ala Arg Met Trp Trp Tyr Phe Gly Cys Tyr Phe Cys Leu
305 310 315 320

Pro Ile Leu Phe Thr Val Thr Cys Gln Leu Val Thr Trp Arg Val Arg
325 330 335

Gly Pro Pro Gly Arg Lys Ser Glu Cys Arg Ala Ser Lys His Glu Gln
340 345 350

Cys Glu Ser Gln Leu Asn Ser Thr Val Val Gly Leu Thr Val Val Tyr
355 360 365

Ala Phe Cys Thr Leu Pro Glu Asn Val Cys Asn Ile Val Val Ala Tyr
370 375 380

Leu Ser Thr Glu Leu Thr Arg Gln Thr Leu Asp Leu Leu Gly Leu Ile
385 390 395 400

Asn Gln Phe Ser Thr Phe Phe Lys Gly Ala Ile Thr Pro Val Leu Leu
405 410 415

Leu Cys Ile Cys Arg Pro Leu Gly Gln Ala Phe Leu Asp Cys Cys Cys
420 425 430

Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala
435 440 445

Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr
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Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro
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<212> DNA
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<211> 29
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<210> 21
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<210> 23
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<210> 28
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<210> 35
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33

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<212> DNA
<213> Unknown

<220>
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36

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<212> DNA
<213> Unknown

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31

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<400> 52
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31

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<210> 54
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33

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 <212> DNA
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<220>
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27

<210> 58

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Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Ser Ala Ile Leu Pro Phe
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Arg Met Val Ser Val Ala Met Arg Glu Lys Trp Pro Phe Gly Ser Phe
85 90 95

Leu Cys Lys Leu Val His Val Met Ile Asp Ile Asn Leu Phe Val Ser
100 105 110

Val Tyr Leu Ile Thr Ile Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
115 120 125

His Pro Ala Trp Ala Gln Asn His Arg Thr Met Ser Leu Ala Lys Arg
130 135 140

Val Met Thr Gly Leu Trp Ile Phe Thr Ile Val Leu Thr Leu Pro Asn
145 150 155 160

Phe Ile Phe Trp Thr Thr Ile Ser Thr Thr Asn Gly Asp Thr Tyr Cys
165 170 175

Ile Phe Asn Phe Ala Phe Trp Gly Asp Thr Ala Val Glu Arg Leu Asn
180 185 190

Val Phe Ile Thr Met Ala Lys Val Phe Leu Ile Leu His Phe Ile Ile
195 200 205

Gly Phe Ser Val Pro Met Ser Ile Ile Thr Val Cys Tyr Gly Ile Ile
210 215 220

Ala Ala Lys Ile His Arg Asn His Met Ile Lys Ser Ser Arg Pro Lys
225 230 235 240

Arg Val Phe Ala Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
245 250 255

Tyr Glu Leu Ile Gly Ile Leu Met Ala Val Trp Leu Lys Glu Met Leu
260 265 270

Leu Asn Gly Lys Tyr Lys Ile Ile Leu Val Leu Ile Asn Pro Thr Ser
 275 280 285

Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Ile Leu Tyr Val Phe
 290 295 300

Met Gly Arg Asn Phe Gln Glu Arg Leu Ile Arg Ser Leu Pro Thr Ser
 305 310 315 320

Leu Glu Arg Ala Leu Thr Glu Val Pro Asp Ser Ala Gln Thr Ser Asn
 325 330 335

Thr Asp Thr Thr Ser Ala Ser Pro Pro Glu Glu Thr Glu Leu Gln Ala
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 <213> Unknown

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 acctgcatca ctgtggatcg ttctattgta gtggttaagg ccaccaaggc ctacaaccag 420
 caagccaaga ggatgacctg gggcaaggtc accagcttgc tcatctgggt gatatccctg 480
 ctggtttcct tgccccaaat tatctatggc aatgtcttta atctcgacaa gctcatatgt 540
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aaacttgtga aggacattgg ttgcctccct taccttgggg totcacatca atggaaatct 960
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<210> 65
<211> 342
<212> PRT
<213> Unknown

<220>
<223> Novel Sequence

<400> 65

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Asp Ser Ser Gln Glu Glu His Gln Ala Phe Leu Gln Phe Ser Lys Val
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Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly
35 40 45

Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
50 55 60

Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
65 70 75 80

Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
85 90 95

Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
100 105 110

Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
115 120 125

Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
130 135 140

Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
145 150 155 160

Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
165 170 175

Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
180 185 190

Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
195 200 205

Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
210 215 220

Gln Lys His Arg Ser Lys Lys Ile Ile Phe Leu Val Met Ala Val Phe
225 230 235 240

Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
245 250 255

His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
260 265 270

Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
275 280 285

Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
290 295 300

Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
305 310 315 320

Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala
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Thr Ser Met Phe Gln Leu
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<210> 66
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<212> DNA

<213> Unknown

<220>

<223> Novel Sequence

<400> 66

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tcaacggcac ccgagctaag tgatgaccgg cgctatgact tcttctctcg cgtggtgccca      600
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cgaagcttca aggcggtagt cacagcagcc accatgtcat cgaggctgtc acacaaaccc 2640
agtgcagac ccaacggtga ggcaaagacc gagctctgtg aaaacgtaga cccaaacagc 2700
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 <211> 915
 <212> PRT
 <213> Unknown

<220>
 <223> Novel Sequence

<400> 67

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245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
450 455 460

Val	Met	Phe	Asn	Lys	Asn	Gly	Asp	Ala	Pro	Gly	Arg	Tyr	Asp	Ile	Phe
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485 490 495

Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly
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Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys
515 520 525

Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr
530 535 540

Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys
545 550 555 560

Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys
565 570 575

Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Ser Ala Val
580 585 590

Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val
595 600 605

Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser
610 615 620

Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr
625 630 635 640

Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser
645 650 655

Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala
660 665 670

Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys
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Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
690 695 700

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 <212> DNA
 <213> Unknown

<220>
 <223> Novel Sequence

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<210> 69
<211> 915
<212> PRT
<213> Unknown

<220>
<223> Novel Sequence

<400> 69

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Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
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Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
450 455 460

Val Met Phe Asn Lys Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe

465					470					475					480
Gln	Tyr	Gln	Thr	Thr	Asn	Thr	Ser	Asn	Pro	Gly	Tyr	Arg	Leu	Ile	Gly
				485					490					495	
Gln	Trp	Thr	Asp	Glu	Leu	Gln	Leu	Asn	Ile	Glu	Asp	Met	Gln	Trp	Gly
			500					505					510		
Lys	Gly	Val	Arg	Glu	Ile	Pro	Ala	Ser	Val	Cys	Thr	Leu	Pro	Cys	Lys
		515					520					525			
Pro	Gly	Gln	Arg	Lys	Lys	Thr	Gln	Lys	Gly	Thr	Pro	Cys	Cys	Trp	Thr
	530					535					540				
Cys	Glu	Pro	Cys	Asp	Gly	Tyr	Gln	Tyr	Gln	Phe	Asp	Glu	Met	Thr	Cys
545					550					555					560
Gln	His	Cys	Pro	Tyr	Asp	Gln	Arg	Pro	Asn	Glu	Asn	Arg	Thr	Gly	Cys
				565					570					575	
Gln	Asp	Ile	Pro	Ile	Ile	Lys	Leu	Glu	Trp	His	Ser	Pro	Trp	Ala	Val
			580					585					590		
Ile	Pro	Val	Phe	Leu	Ala	Met	Leu	Gly	Ile	Ile	Ala	Thr	Ile	Phe	Val
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Met	Ala	Thr	Phe	Ile	Arg	Tyr	Asn	Asp	Thr	Pro	Ile	Val	Arg	Ala	Ser
	610					615					620				
Gly	Arg	Glu	Leu	Ser	Tyr	Val	Leu	Leu	Thr	Gly	Ile	Phe	Leu	Cys	Tyr
625					630					635					640
Ile	Ile	Thr	Phe	Leu	Met	Ile	Ala	Lys	Pro	Asp	Val	Ala	Val	Cys	Ser
				645					650					655	
Phe	Arg	His	Val	Phe	Leu	Gly	Leu	Gly	Met	Cys	Ile	Ser	Tyr	Ala	Ala
			660					665					670		
Leu	Leu	Thr	Lys	Thr	Asn	Arg	Ile	Tyr	Arg	Ile	Phe	Glu	Gln	Gly	Lys
		675					680					685			
Lys	Ser	Val	Thr	Ala	Pro	Arg	Leu	Ile	Ser	Pro	Thr	Ser	Gln	Leu	Ala
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<210> 70
 <211> 2748
 <212> DNA
 <213> Unknown

<220>
 <223> Novel Sequence

<400> 70
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 cactcaatcc ggatcgaggg ggacgtcacc ctcggggggc tgttccccgt gcacgccaag 180
 ggtcccagcg gagtgccttg cggcgacatc aagagggaaa acgggatcca caggctggaa 240
 gcgatgctct acgccctgga ccagatcaac agtgatccca acctactgcc caacgtgacg 300
 ctgggcgcgc ggatcctgga cacttgttcc agggacactt acgcgctoga acagtcgctt 360
 actttcgtcc aggcgctcat ccagaaggac acctccgacg tgcgctgcac caacggcgaa 420
 ccgccggttt tcgtcaagcc ggagaaagta gttggagtga ttggggcttc ggggagttcg 480
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 tcaaaaaaag aagacacaga tcgcaaagtc acaggacagg agagaattgg aaaagattcc 1200
 aactatgagc aggagggtaa agtccagttc gtgattgacg cagtctatgc tatggctcac 1260
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tcagtgtgca	cactaccatg	taagccagga	cagagaaaga	agacacagaa	aggaactcct	1620
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agtgacagac	ccaacggtga	ggcaaagacc	gagctctgtg	aaaacgtaga	cccaaacagc	2700
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<210>	71
<211>	915
<212>	PRT
<213>	Unknown

<220>
<223> Novel Sequence

<400> 71

Met Val Gln Leu Arg Lys Leu Leu Arg Val Leu Thr Leu Met Lys Phe

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Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp	35	40	45
Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly	50	55	60
Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu	65	70	75
Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu	85	90	95
Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp	100	105	110
Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln	115	120	125
Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe	130	135	140
Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser	145	150	155
Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln	165	170	175
Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr	180	185	190
Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala	195	200	205
Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu	210	215	220
Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln	225	230	235
			240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro
450 455 460

Lys Ser Val Thr Ala Pro Arg Leu Ile Ser Pro Thr Ser Gln Leu Ala
690 695 700

Ile Thr Ser Ser Leu Ile Ser Val Gln Leu Leu Gly Val Phe Ile Trp
705 710 715 720

Phe Gly Val Asp Pro Pro Asn Ile Ile Ile Asp Tyr Asp Glu His Lys
725 730 735

Thr Met Asn Pro Glu Gln Ala Arg Gly Val Leu Lys Cys Asp Ile Thr
740 745 750

Asp Leu Gln Ile Ile Cys Ser Leu Gly Tyr Ser Ile Leu Leu Met Val
755 760 765

Thr Cys Cys Val Tyr Ala Ile Lys Thr Arg Gly Val Pro Glu Asn Phe
770 775 780

Asn Glu Ala Lys Pro Ile Gly Phe Thr Met Tyr Thr Thr Cys Ile Val
785 790 795 800

Trp Leu Ala Phe Ile Pro Ile Phe Phe Gly Thr Ala Gln Ser Ala Glu
805 810 815

Lys Leu Tyr Ile Gln Thr Thr Thr Leu Thr Ile Ser Met Asn Leu Ser
820 825 830

Ala Ser Val Ala Leu Gly Met Leu Tyr Met Pro Lys Val Tyr Ile Ile
835 840 845

Ile Phe His Pro Glu Leu Asn Val Gln Lys Arg Lys Arg Ser Phe Lys
850 855 860

Ala Val Val Thr Ala Ala Thr Met Ser Ser Arg Leu Ser His Lys Pro
865 870 875 880

Ser Asp Arg Pro Asn Gly Glu Ala Lys Thr Glu Leu Cys Glu Asn Val
885 890 895

Asp Pro Asn Ser Pro Ala Ala Lys Lys Lys Tyr Val Ser Tyr Asn Asn
900 905 910

Leu Val Ile

<210> 72
 <211> 2748
 <212> DNA
 <213> Unknown

<220>
 <223> Novel Sequence

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 cactcaatcc ggatcgaggg ggacgtcacc ctcggggggc tgttccccgt gcacgccaag 180
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 ctgggcgcgc ggatcctgga cacttgttcc agggacactt acgcgctcga acagtcgctt 360
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<210> 73
<211> 915
<212> PRT
<213> Unknown

<220>
<223> Novel Sequence

<400> 73

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Arg Gly Gln Glu Met Tyr Ala Pro His Ser Ile Arg Ile Glu Gly Asp
35 40 45

Val Thr Leu Gly Gly Leu Phe Pro Val His Ala Lys Gly Pro Ser Gly
50 55 60

Val Pro Cys Gly Asp Ile Lys Arg Glu Asn Gly Ile His Arg Leu Glu
65 70 75 80

Ala Met Leu Tyr Ala Leu Asp Gln Ile Asn Ser Asp Pro Asn Leu Leu
85 90 95

Pro Asn Val Thr Leu Gly Ala Arg Ile Leu Asp Thr Cys Ser Arg Asp
100 105 110

Thr Tyr Ala Leu Glu Gln Ser Leu Thr Phe Val Gln Ala Leu Ile Gln
115 120 125

Lys Asp Thr Ser Asp Val Arg Cys Thr Asn Gly Glu Pro Pro Val Phe
130 135 140

Val Lys Pro Glu Lys Val Val Gly Val Ile Gly Ala Ser Gly Ser Ser
145 150 155 160

Val Ser Ile Met Val Ala Asn Ile Leu Arg Leu Phe Gln Ile Pro Gln
165 170 175

Ile Ser Tyr Ala Ser Thr Ala Pro Glu Leu Ser Asp Asp Arg Arg Tyr
180 185 190

Asp Phe Phe Ser Arg Val Val Pro Pro Asp Ser Phe Gln Ala Gln Ala
195 200 205

Met Val Asp Ile Val Lys Ala Leu Gly Trp Asn Tyr Val Ser Thr Leu
210 215 220

Ala Ser Glu Gly Ser Tyr Gly Glu Lys Gly Val Glu Ser Phe Thr Gln
225 230 235 240

Ile Ser Lys Glu Ala Gly Gly Leu Cys Ile Ala Gln Ser Val Arg Ile
245 250 255

Pro Gln Glu Arg Lys Asp Arg Thr Ile Asp Phe Asp Arg Ile Ile Lys
260 265 270

Gln Leu Leu Asp Thr Pro Asn Ser Arg Ala Val Val Ile Phe Ala Asn
275 280 285

Asp Glu Asp Ile Lys Gln Ile Leu Ala Ala Ala Lys Arg Ala Asp Gln
290 295 300

Val Gly His Phe Leu Trp Val Gly Ser Asp Ser Trp Gly Ser Lys Ile
305 310 315 320

Asn Pro Leu His Gln His Glu Asp Ile Ala Glu Gly Ala Ile Thr Ile
325 330 335

Gln Pro Lys Arg Ala Thr Val Glu Gly Phe Asp Ala Tyr Phe Thr Ser
340 345 350

Arg Thr Leu Glu Asn Asn Arg Arg Asn Val Trp Phe Ala Glu Tyr Trp
355 360 365

Glu Glu Asn Phe Asn Cys Lys Leu Thr Ile Ser Gly Ser Lys Lys Glu
370 375 380

Asp Thr Asp Arg Lys Cys Thr Gly Gln Glu Arg Ile Gly Lys Asp Ser
385 390 395 400

Asn Tyr Glu Gln Glu Gly Lys Val Gln Phe Val Ile Asp Ala Val Tyr
405 410 415

Ala Met Ala His Ala Leu His His Met Asn Lys Asp Leu Cys Ala Asp
420 425 430

Tyr Arg Gly Val Cys Pro Glu Met Glu Gln Ala Gly Gly Lys Lys Leu
435 440 445

Leu Lys Tyr Ile Arg Asn Val Asn Phe Asn Gly Ser Ala Gly Thr Pro

450	455	460																	
Val Met Phe Asn Lys	Asn Gly Asp Ala Pro Gly Arg Tyr Asp Ile Phe																		
465	470	475																	480
Gln Tyr Gln Thr Thr	Asn Thr Ser Asn Pro Gly Tyr Arg Leu Ile Gly																		
	485	490																	495
Gln Trp Thr Asp Glu Leu Gln Leu Asn Ile Glu Asp Met Gln Trp Gly																			
	500	505																	510
Lys Gly Val Arg Glu Ile Pro Ala Ser Val Cys Thr Leu Pro Cys Lys																			
	515	520																	525
Pro Gly Gln Arg Lys Lys Thr Gln Lys Gly Thr Pro Cys Cys Trp Thr																			
	530	535																	540
Cys Glu Pro Cys Asp Gly Tyr Gln Tyr Gln Phe Asp Glu Met Thr Cys																			
	545	550																	560
Gln His Cys Pro Tyr Asp Gln Arg Pro Asn Glu Asn Arg Thr Gly Cys																			
	565	570																	575
Gln Asp Ile Pro Ile Ile Lys Leu Glu Trp His Ser Pro Trp Ala Val																			
	580	585																	590
Ile Pro Val Phe Leu Ala Met Leu Gly Ile Ile Ala Thr Ile Phe Val																			
	595	600																	605
Met Ala Thr Phe Ile Arg Tyr Asn Asp Thr Pro Ile Val Arg Ala Ser																			
	610	615																	620
Gly Arg Glu Leu Ser Tyr Val Leu Leu Thr Gly Ile Phe Leu Cys Tyr																			
	625	630																	640
Ile Ile Thr Phe Leu Met Ile Ala Lys Pro Asp Val Ala Val Cys Ser																			
	645	650																	655
Phe Arg Arg Val Phe Leu Gly Leu Gly Met Cys Ile Ser Tyr Ala Ala																			
	660	665																	670
Leu Leu Thr Lys Thr Asn Arg Ile Tyr Arg Ile Phe Glu Gln Gly Lys																			
	675	680																	685

Leu Val Ile
915

<210> 74
<211> 1842
<212> DNA
<213> Unknown

<220>
<223> Novel Sequence

<400> 74
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ggggagagct gtgcacctac agtgatccag cgccgcggca gggacgcctg gggaccggga 180
aattctgcaa gagacgttct gcgagcccga gcaccaggag aggagcaggg ggcagcgttt 240
cttgcgggac cctcctggga cctgccggcg gcccggggcc gtgaccgggc tgcaggcaga 300
ggggcgagg cgtcggcagc cggacccccg ggacctcaa ccaggccacc tggcccctgg 360
aggtgaaaag gtgctcgggg tcaggagcct tctgaaactt tggggagagg gaacccacg 420
gccctccagc tcttcttca gatctcagag gaggaagaga agggctccag aggcgctggc 480
atttcggggc gtagccagga gcagagtgtg aagacagtcc ccggagccag cgatcttttt 540
tactggccaa ggagagccgg gaaactccag ggttcccacc acaagcccct gtccaagacg 600
gccaatggac tggcggggca cgaagggtgg acaattgcac tcccgggccc ggcgctggcc 660
cagaatggat ctttgggtga aggaatccat gagcctgggg gtccccgccg gggaaacagc 720
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gccaacctgg ctttctggga ctttctcacc atcttcttct gccttcgct ggtcatcttc 960
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gccaaacttg ctgttatatg ggtgggagct ctattgttag caattccaga agttgttctc 1200
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gcgagactgt ggtggtatTT tggctgttac ttttgtttgc ccacgctttt caccatcacc 1380
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 atggagtgct gctgctgttg ctgtgaggaa tgcattcaga agtcttcaac ggtgaccagt 1740
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 cgtgaaatgt ccacttttgc ttctgtcgga actcattgct ga 1842

<210> 75
 <211> 613
 <212> PRT
 <213> Unknown
 <220>
 <223> Novel Sequence
 <400> 75

Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro
 20 25 30

Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val
 35 40 45

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
 50 55 60

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
 65 70 75 80

Leu Ala Gly Pro Ser Trp Asp Leu Pro Ala Ala Pro Gly Arg Asp Pro
 85 90 95

Ala Ala Gly Arg Gly Ala Glu Ala Ser Ala Ala Gly Pro Pro Gly Pro
 100 105 110

Pro Thr Arg Pro Pro Gly Pro Trp Arg Trp Lys Gly Ala Arg Gly Gln
115 120 125

Glu Pro Ser Glu Thr Leu Gly Arg Gly Asn Pro Thr Ala Leu Gln Leu
130 135 140

Phe Leu Gln Ile Ser Glu Glu Glu Glu Lys Gly Pro Arg Gly Ala Gly
145 150 155 160

Ile Ser Gly Arg Ser Gln Glu Gln Ser Val Lys Thr Val Pro Gly Ala
165 170 175

Ser Asp Leu Phe Tyr Trp Pro Arg Arg Ala Gly Lys Leu Gln Gly Ser
180 185 190

His His Lys Pro Leu Ser Lys Thr Ala Asn Gly Leu Ala Gly His Glu
195 200 205

Gly Trp Thr Ile Ala Leu Pro Gly Arg Ala Leu Ala Gln Asn Gly Ser
210 215 220

Leu Gly Glu Gly Ile His Glu Pro Gly Gly Pro Arg Arg Gly Asn Ser
225 230 235 240

Thr Asn Arg Arg Val Arg Leu Lys Asn Pro Phe Tyr Pro Leu Thr Gln
245 250 255

Glu Ser Tyr Gly Ala Tyr Ala Val Met Cys Leu Ser Val Val Ile Phe
260 265 270

Gly Thr Gly Ile Ile Gly Asn Leu Ala Val Met Cys Ile Val Cys His
275 280 285

Asn Tyr Tyr Met Arg Ser Ile Ser Asn Ser Leu Leu Ala Asn Leu Ala
290 295 300

Phe Trp Asp Phe Leu Ile Ile Phe Phe Cys Leu Pro Leu Val Ile Phe
305 310 315 320

His Glu Leu Thr Lys Lys Trp Leu Leu Glu Asp Phe Ser Cys Lys Ile
325 330 335

575

Val Gly Thr His Cys
610

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<210> 76
<211> 1842
<212> DNA
<213> Homo sapiens
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<400>	76						
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aattctgcaa	gagacgttct	gcgagcccga	gcaccacagg	aggagcagg	ggcagcgttt		240
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atttcggggc	gtagccagga	gcagagtgtg	aagacagtcc	cggagccag	cgatcttttt		540
tactggccaa	ggagagccgg	gaaactccag	ggttcccacc	acaagcccct	gtccaagacg		600
gccaatggac	tggcggggca	cgaagggtgg	acaattgcac	tcccggggcg	ggcgctggcc		660
cagaatggat	ccttgggtga	aggaatccat	gagcctgggg	gtccccgcg	gggaaacagc		720
acgaaccggc	gtgtgagact	gaagaacccc	ttctaccgc	tgaccacagga	gtcctatgga		780
gcctacgcgg	tcatgtgtct	gtccgtggtg	atcttcggga	cggcgcacat	tggcaacctg		840
gcggtgatgt	gcctcgtgtg	ccacaactac	tacatgcgga	gcctctccaa	ctccctcttg		900
gccaacctgg	ccttctggga	ctttctcctc	atcttcttct	gccttccgct	ggctcatcttc		960
cacgagctga	ccaagaagtg	gctgctggag	gacttctcct	gcaagatcgt	gcctatatata		1020
gaggtcgctt	ctctgggagt	caccaccttc	accttatgtg	ctctgtgcat	agaccgcttc		1080


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cgtgctgcc ccaacgtaca gatgtactac gaaatgatcg aaaactgttc ctcaacaact 1140
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cgccagctga gcaaggagga tttgggggtt agtggccgag ctccggcaga aaggtgcatt 1260
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```

```

<210> 77
<211> 613
<212> PRT
<213> Unknown

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<220>
<223> Novel Sequence

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<400> 77

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```

Met Arg Ala Pro Gly Ala Leu Leu Ala Arg Met Ser Arg Leu Leu Leu
1          5          10          15

```

```

Leu Leu Leu Leu Lys Val Ser Ala Ser Ser Ala Leu Gly Val Ala Pro
20          25          30

```

```

Ala Ser Arg Asn Glu Thr Cys Leu Gly Glu Ser Cys Ala Pro Thr Val
35          40          45

```

```

Ile Gln Arg Arg Gly Arg Asp Ala Trp Gly Pro Gly Asn Ser Ala Arg
50          55          60

```

```

Asp Val Leu Arg Ala Arg Ala Pro Arg Glu Glu Gln Gly Ala Ala Phe
65          70          75          80

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305		310		315		320
His Glu Leu Thr	Lys Lys Trp Leu Leu	Glu Asp Phe Ser Cys	Lys Ile			
	325		330		335	
Val Pro Tyr Ile	Glu Val Ala Ser Leu	Gly Val Thr Thr	Phe Thr Leu			
	340		345		350	
Cys Ala Leu Cys	Ile Asp Arg Phe Arg	Ala Ala Thr Asn	Val Gln Met			
	355		360		365	
Tyr Tyr Glu Met	Ile Glu Asn Cys Ser	Ser Thr Thr Ala	Lys Leu Ala			
	370		375		380	
Val Ile Trp Val	Gly Ala Leu Leu Leu	Ala Leu Pro Glu	Val Val Leu			
	385		390		395	
Arg Gln Leu Ser	Lys Glu Asp Leu Gly	Phe Ser Gly Arg	Ala Pro Ala			
	405		410		415	
Glu Arg Cys Ile	Ile Lys Ile Ser Pro	Asp Leu Pro Asp	Thr Ile Tyr			
	420		425		430	
Val Leu Ala Leu	Thr Tyr Asp Ser Ala	Arg Leu Trp Trp	Tyr Phe Gly			
	435		440		445	
Cys Tyr Phe Cys	Leu Pro Thr Leu Phe	Thr Ile Thr Cys	Ser Leu Val			
	450		455		460	
Thr Ala Arg Lys	Ile Arg Lys Ala Glu	Lys Ala Cys Thr	Arg Gly Asn			
	465		470		475	
Lys Arg Gln Ile	Gln Leu Glu Ser Gln	Met Asn Cys Thr	Val Val Ala			
	485		490		495	
Leu Thr Ile Leu	Tyr Gly Phe Cys Ile	Ile Pro Glu Asn	Ile Cys Asn			
	500		505		510	
Ile Val Thr Ala	Tyr Met Ala Thr Gly	Val Ser Gln Gln	Thr Met Asp			
	515		520		525	
Leu Leu Asn Ile	Ile Ser Gln Phe Leu	Leu Phe Phe Lys	Ser Tyr Val			
	530		535		540	

Thr Pro Val Leu Leu Phe Cys Leu Cys Lys Pro Phe Ser Arg Ala Phe
545 550 555 560

Met Glu Cys Cys Cys Cys Cys Cys Glu Glu Cys Ile Gln Lys Ser Ser
565 570 575

Thr Val Thr Ser Asp Asp Asn Asp Asn Glu Tyr Thr Thr Glu Leu Glu
580 585 590

Leu Ser Pro Phe Ser Thr Ile Arg Arg Glu Met Ser Thr Phe Ala Ser
595 600 605

Val Gly Thr His Cys
610

<210> 78
<211> 1086
<212> DNA
<213> Unknown

<220>
<223> Novel Sequence

<400> 78
atgtcccctg aatgcgcgcg ggcagcgggc gacgcgccct tgcgcagcct ggagcaagcc 60
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gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgtgctggg caacgtgtgc 180
gccctggtgc tggtaggcgc cgcacgacgc cgcggcgcga ctgcctgcct ggtactcaac 240
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 tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
 gaaaaggagg ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
 ggctaa 1086

<210> 79
 <211> 361
 <212> PRT
 <213> Unknown

<220>
 <223> Novel Sequence

<400> 79

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
 1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
 20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
 35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
 50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
 65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
 85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
 100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
 115 120 125

Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
 130 135 140

<210> 80
 <211> 1086
 <212> DNA
 <213> Unknown

<220>
 <223> Novel Sequence

<400> 80
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 gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc 180
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 ctacaggtaa gcttggccta ctcgagagc caccagatcc gcgtgtccca gcaggacttc 780
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 tccctcttct tctgggtggg ggccttcaca tttgctaatt cagccctaaa ccccatcctc 960
 tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
 gaaaaggag ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
 ggctaa 1086

<210> 81
 <211> 361
 <212> PRT
 <213> Unknown

<220>
 <223> Novel Sequence

<400> 81

Met Ser Pro Glu Cys Ala Arg Ala Ala Gly Asp Ala Pro Leu Arg Ser
1 5 10 15

Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
20 25 30

Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
35 40 45

Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
50 55 60

Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65 70 75 80

Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
85 90 95

Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
100 105 110

Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
115 120 125

Leu Ala Ala Val Ser Leu Asn Arg Met Val Cys Ile Val His Leu Gln
130 135 140

Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145 150 155 160

Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
165 170 175

Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
180 185 190

Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
195 200 205

Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220

Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240

Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255

Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270

Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
275 280 285

Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
290 295 300

Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305 310 315 320

Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
325 330 335

Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
340 345 350

Arg Asn Asp Leu Ser Ile Ile Ser Gly
355 360

<210> 82
<211> 1212
<212> DNA
<213> Unknown

<220>
<223> Novel Sequence

<400> 82
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aactaccct tctgctggg cgttggtggc tgctatttcc gcacgctact gtttgagatg 360

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gtctgcctgg cctcagtgt caacgtcact gccctgagcg tggaaacgcta tgtggccgtg 420
gtgcacccac tccaggccag gtccatggtg acgcgggccc atgtgcgcgc agtgcttggg 480
gccgtctggg gtcttgccat gctctgtccc ctgccaaca ccagcctgca cggcatccgg 540
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cacagctccc acagcctcag caggatgacc acaggcagca ccctgtgtga tgtgggctcc 1140
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gatccatcct ga 1212

```

```

<210> 83
<211> 403
<212> PRT
<213> Unknown

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<220>
<223> Novel Sequence
<400> 83

```

```

Met Ala Cys Asn Gly Ser Ala Ala Arg Gly His Phe Asp Pro Glu Asp
1           5           10           15

```

```

Leu Asn Leu Thr Asp Glu Ala Leu Arg Leu Lys Tyr Leu Gly Pro Gln
          20           25           30

```

```

Gln Thr Glu Leu Phe Met Pro Ile Cys Ala Thr Tyr Leu Leu Ile Phe
          35           40           45

```

```

Val Val Gly Ala Val Gly Asn Gly Leu Thr Cys Leu Val Ile Leu Arg
          50           55           60

```


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 caggactctc tgtgcgtgac cctgcctaa 930

<210> 85
 <211> 309
 <212> PRT
 <213> Unknown

 <220>
 <223> Novel Sequence

 <400> 85

Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
 1 5 10 15

Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
 20 25 30

Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
 35 40 45

Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
 50 55 60

Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
 65 70 75 80

Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
 85 90 95

Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val
 100 105 110

Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
 115 120 125

<400> 86
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35 40 45

Glu Asp Glu Glu Ala Lys Gly Val Gln Gln Tyr Val Pro Glu Glu Trp
50 55 60

Ala Glu Tyr Pro Arg Pro Ile His Pro Ala Gly Leu Gln Pro Thr Lys
65 70 75 80

Pro Leu Val Ala Thr Ser Pro Asn Pro Asp Lys Asp Gly Gly Thr Pro
85 90 95

Asp Ser Gly Gln Glu Leu Arg Gly Asn Leu Thr Gly Ala Pro Gly Gln
100 105 110

Arg Leu Gln Ile Gln Asn Pro Leu Tyr Pro Val Thr Glu Ser Ser Tyr
115 120 125

Ser Ala Tyr Ala Ile Met Leu Leu Ala Leu Val Val Phe Ala Val Gly
130 135 140

Ile Val Gly Asn Leu Ser Val Met Cys Ile Val Trp His Ser Tyr Tyr
145 150 155 160

Leu Lys Ser Ala Trp Asn Ser Ile Leu Ala Ser Leu Ala Leu Trp Asp
165 170 175

Phe Leu Val Leu Phe Phe Cys Leu Pro Ile Val Ile Phe Asn Glu Ile
180 185 190

Thr Lys Gln Arg Leu Leu Gly Asp Val Ser Cys Arg Ala Val Pro Phe
195 200 205

Cys Cys Cys Cys Glu Glu Cys Gly Gly Ala Ser Glu Ala Ser Ala Ala
 435 440 445

Asn Gly Ser Asp Asn Lys Leu Lys Thr Glu Val Ser Ser Ser Ile Tyr
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Phe His Lys Pro Arg Glu Ser Pro Pro Leu Leu Pro Leu Gly Thr Pro
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Cys

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<210> 89
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<400> 93

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Gly Val Ser Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Leu Leu His
20          25          30

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Ser Ala Asp Ile Arg Arg Gln Ala Pro Ala Leu Phe Thr Leu Asn Leu
35          40          45

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Thr Cys Gly Asn Leu Leu Cys Thr Val Val Asn Met Pro Leu Thr Leu
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Ala Gly Val Val Ala Gln Arg Gln Pro Ala Gly Asp Arg Leu Cys Arg
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<210> 100
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32